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Genetic Studies on Amylose Content and Amylographic Breakdown Viscosity of Milled Rice by Means of Generation Mean Analysis[1]

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Abstract : Amylose content and amylographic breakdown viscosity are important parameters for predicting eating and processing quality of rice. A total of 6 populations, P_1, P_2, F_1, F_2, BC_1 and BC_2, derived from two rice cultivars Guichow and Lemont, were used as experimental materials to elucidate the genetic information about the two endosperm characteristics. Genetic mechanism of two studied endosperm characteristics deduced from generation mean analysis were different. An additive-dominance genetic model was perfectly adequate to describe the amylose content data set, and inadequate to the data set of amylographic breakdown viscosity. Conclusion inferred suggested that amylose content of milled rice was mainly controlled by additive gene effect although dominant gene effect was also involved. Furthermore, the gene producing high amylose content was dominant. On the other hand. additive, dominant and additive×dominant interaction were involved to differentiate the level of amylographic breakdown viscosity among materials studied and additive and dominant gene effects were more or less equal. It was also found that low amylographic breakdown viscosity was dominant. A genetic hypothesis deduced from the distribution observation and Chi-square test indicated that a segregation ratio resulting from one single incompletely dominance gene in controlling amylose content was confirmed, and, however, was not confirmed in differentiating amylographic breakdown viscosity.

Key words : Amylose content, Amylographic breakdown viscosity, Milled rice, Generation mean.

INTRODUCTION

Webb and Stermer[47] surveyed some of the most important physico-chemical properties in rice, and concluded that the starch components of milled rice, particularly the

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amylose content or amylose: amylopection ratio, its temperature of gelatinization, and its pasting characteristics, were largely responsible for the major differences in rice cooking and processing behavior. It is well recognized that among those components, amylose content of milled rice, a chemical property of rice grains, is one of the most important attributes for predicting the cooking, eating and processing characteristics[16,31,47,48]. Basically, cultivars with a low a amylose content cook moist, sticky, and tender. Cultivars with a high amylose content cook dry, fluffy, and become hand upon cooling. Whereas, the ones with an intermediate amylose content cook tender, fluffy, and do not become hand upon cooling[14,15,43]. On the other hand, the amylographic pasting characteristics of milled rice determined with the Brabender Visco/Amylograph, a physical property of rice strch showed appreciable differences among cultivars of known cooking and processing behaviors[47]. Simply because cultivars with a relatively low a amylographic breakdown viscosity showed low loss of solids and little splitting and fraying of edges and ends in canning[47], scientists in the US. considered that amylographic viscosity measurements were particularly useful in evaluating cultivars for superior parboil-canning characteristics and quick-cooking properties[47]. Rice scientists in Japan suggested that amylographic breakdown viscosity could be used as an index factor for palatability evaluation[37]. Published results from Taiwan indicated that a highly significant correlation existed between amylographic breakdown viscosity and eating quality[26].

Since the regular amylographic test was time-consuming, Webb et al.[42] had proposed an abridged amylographic method, starting the run at 60°C, concluding it after 10 minutes of cooking at 90°C, and concentrating mainly on amylographic breakdown viscosity after 10 minutes cooking. However, because both regular and abridged amylographic tests were all based on 50g of ground rice samples, they were difficult to apply in the testing of early segregating populations such as F_2, backcoross F_1, and/or backcross F_2, based on the single plant basis. Thus, it was impossible to conduct a genetic studies on amylographic breakdown viscosity form these segregating generations using a single plant as an measurement unit. A new method derived form abridged amylographic test was developed by the authors at the Reginal Rice Quality Laboratory, USDA, in 1990. Since the new small-sample size modified abridged amylographic test requires only 10g of ground rice flour, genetic studies on amylographic breakdown viscosity, based on single plant basis, were then possible[19].

In this paper, the genetic studies on amylographic breakdown viscosity, using small-sample size modified abridged amylographic test, and amylose content, based on bulk sample basis, of milled rice, are presented.

MATERIALS AND METHODS

Two rice cultivars, Guichow and Lemont, with different amylose content and amylographic profiles, were used in this experiment. The required crosses were made. Thus, the P_1, P_2, F_1, F_2, B_1F_1, and B_2F_1 populations were transplanted and cultivated in a flooded paddy field of the Texas A&M University Agricultural Research and Extension Center near Beaumont, Texas, in a randomized complete block design with two replications. Each block

contained one plot of P_1, P_2, and F_1, two plots of B_1F_1 and B_2F_1,and seven plots of F_2 plants. Each three-row plot included 30 plants spaced at 30×30cm. Each plant was harvested and processed individually.

Amylographic breakdown viscosity was determined by the new small-Sample size abridged amylograph test innovated by the authors at the Regional Rice Quality Laboratory, USDA, in 1991, an unpublished method. Basically, the new amylographic test described here was derived form the abridged amylographic test innovated by Webb et al.[42]. The procedures are briefly outlined as follows. First, the 700 cm/g sensitivity cartridge used in regular test is replaced by a 250cm/g cartridge. Then, 10g of the ground milled rice sample is blended with 80ml distilled water in a 250ml flask. After blending, (by means of shaking by hand), the rice-water slurry is rapidly transferred into a small Amylo/Visco/Graph bowl (manufactured by C. W. Bradender Instruments Inc. for the rapid amylogram test) and transfer is completely quantitatively with an additional 20ml of distilled water. The final concentration of the slurry in the amylograph cup is 10g of ground milled rice flour in 100ml distilled water, i. e., 10% concentration. In contrast, the traditional amylographic test uses 50g of ground rice flour in 450ml distilled water, i. e., 11.1% concentration. The run is started at 65°C and concluded after 10 minutes of cooking at 95°C. Thus, three basic viscosity measurements, amylographic peak, hot-paste, and cool-paste viscosity and a derivative viscosity, amylographic breakdown viscosity are figured out. A small-sample size abridged amylographic profile for Lemont and Guichow is plotted in Fig. 1.

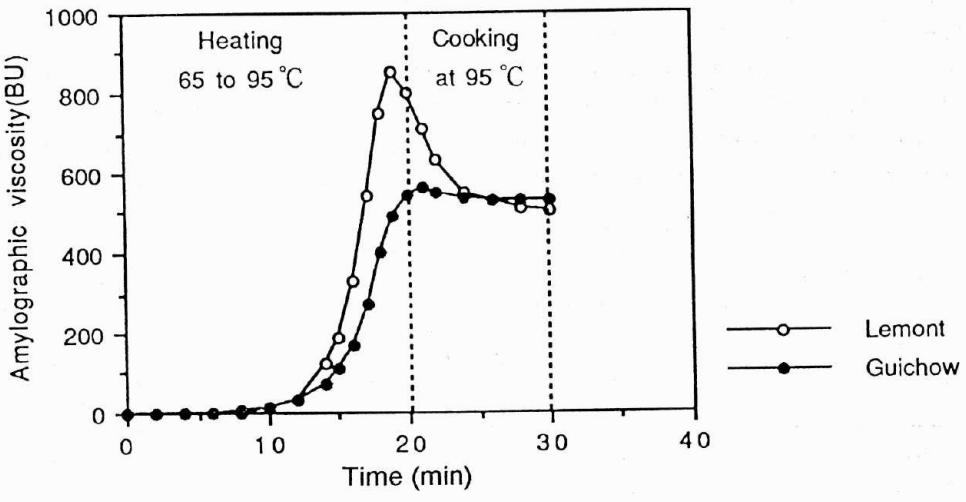

Fig. 1. A small-sample size abridged amylographic profile of Lemont and Guichow rice.

Amylose content of milled rice was analyzed by a totally automated system of amylose analysis in white milled rice innovated by Webb[38]. The procedures are outlined as follows. First, 60mg ground rice sample (passed through 100-mesh sieve, i. e., Udy brass screen

mesh) is transferred quantitatively into sample test tube and 1ml ethanol is added to wet the sample. The sample then is added 6ml 1N NaOH and keeps overnight at room temperature. After bringing the sample up to exactly 60ml volume with 54ml deionized distilled water, the sample is shaken thoroughly with a Vortex shaker. Then, the sample is kept overnight at room temperature again. The sample is shaken thoroughly before starting a run with a Technicon Auto Analyzer (Technicon Instruments Corp., Tarrytown, NY).

The data were analyzed and interpreted on the basis of the biometrical techniques developed by Mather and Jinks[27]. The analysis involoved a test of the additive-dominance effect and six-parameter digenic epistasis model. The estimates of the six parameters are: midparent value (m); additive (d); dominance (h); additive×additive (i); additive×dominance (j); and×dominance×dominance (l) gene effects.

RESULTS

As mentioned previously, amylographic breakdown viscosity, as an endosperm characteristic, is impossible to measure on a single seed basis. All seeds on a plant, then, must be taken as a measurement unit[29]. However, in order to compare and contrast easily, data on amylose content in this study were also analyzed on bulk sample basis although single grain amylose content determination had been developed[38] and some papers had discussed in amylose content genetic model for rice[32,33]. Thus, the limitations and flaws of bulk sample analysis influencing reasonable genetic hypothesis inferred, that were mentioned in author's previous papers[22,23,24,25], existed in this data and should be kept in mind.

Generation Means

Means of amylographic breakdown viscosity and amylose content of milled rice for these six generations and their standard errors of the means were presented in Table 1. It clearly indicated that Lemont had a high amylographic breakdown viscosity and an intermediate amylose content, on the other hand, Guichow showed a relatively low amylographic breakdown viscosity and a high amylose content. Therefore, there was a difference in amylographic breakdown viscosity of about 300 BU between the parents and a difference in amylose content of about 5%.

Table 1. Generation means and the standard errors of the means for amylose content and amylographic breakdown viscosity in the Guichow/Lemont crosses.

Generation	Amylose content(%)		Amylographic breakdown viscosity (BU[z])	
	Mean	Standard error	Mean	Standard error
Guichow(20)[y]	26.7	0.0894	32	3.21
Lemont(20)	21.4	0.1323	330	7.45
F_1(Guichow/Lemont)(20)	25.0	0.0707	107	2.82
F_2(300)	24.4	0.1065	133	5.73
F_1/Guichow(120)	26.0	0.0957	74	6.84
F_1/Lemont(120)	23.3	0.1497	187	5.73

[z] Brabender Units.
[y] Number in each parenthesis indicates the number of plant used for test in each generation.

In the F_1 (Guchow/Lemont), both endosperm characteristics studied were generally intermediate between the two parental means. The mean amylographic breakdown viscosity of the F_1 (20 plants), 107 BU, was about 74 BU lower than that of the mid-parent (181 BU), toward the low amylographic breakdown viscosity parent. On the other hand, the mean amylose content of the F_1, 25%, was about 1% higher than that of the mid-parent (24.1%), toward the high amylose content parent.

Means of two endosperm characteristic from the F_2 plants also lay between the two parental means. The mean amylographic breakdown viscosity of the F_2 (300 plants), 133 BU, showed about 48 BU lower than that of the midparent value (181 BU), toward the low amylographic breakdown viscosity parent. The mean amylose content of the F_2, 24.4%, was approximately equal to that of the midparent (24.1%).

The endosperm characteristics studied of backcross F_1/Guichow were almost intermediate between the two parental means, i. e., Guichow and F_1. The mean amylographic breakdown viscosity of backcross F_1/Guichow, 74 BU, was nearly equal to that of (Guichow $+F_1)/2=(32$ BU$+107$ BU$)/2=70$ BU. Average amylose content of backcross F_1/Guichow was 26% approximately equal to that of (Guichow$+F_1)/2=(26.7\%+25.0\%)/2=25.9\%$.

The characteristics studied of backcross F_1/Lemont lay somewhere between the two parents, Lemont and F_1. The mean amylose content of backcross F_1/Lemont was 23.3% almost equal to that of its midparent, Lemont and F_1, i. e. (Lemont$+F_1)/2=(21.4\%+25\%)/2=23.2\%$. However, average amylographic breakdown viscosity of backcross F_1/Lemont was 187 BU, which was certainly lower than that of its midparent, i. e., (Lemont$+F_1)/2=$ (330BU$+107$ BU$)/2=219$ BU.

From these results mentioned adove, it suggested that different genetic systems were involved in the control of these endosperm characteristics studied. The details will be further discussed in following sections.

The Scaling Test Adequate to the Additive-Dominance Model

As described by Mather and Jinks[27], if generation means depend only on the additive -dominance effects of genes, i. e., there are no interactions between non-allelic genes and no other disturbing factors such as differential viability, differential fertility or other unknown factors, then, it is clearly possible to find simple relationships between the expected values of different generations. For example, the F_2 generation mean under these condition is expected to deviate form the midparent value by half the amount that the F_1 generation mean deviates from the midparent values, the backcross generation mean is expected to deviate from the recurrent parent value by half the amount that the F_1 generation mean deviates from the recurrent parent value, etc. Thus, we can test these predicted relationships between generation means and the expectation that they depend only on the additive -dominance effects of genes. The scaling test mentioned by Mather and Jinks[27], is used in this paper. The quantities, A, B, and C and their standard errors calculated by following the formulae of Mather and Jinks presented in Biometrical Genetics[27] were enumerated in Table 2.

Table 2. The ABC scaling test for amylose content and amylographic breakdown viscosity in the Guichow/Lemont crosses.

	Amylose content		Amylographic breakdown viscosity	
	Value	Standard error of the value	Value	Standard error of the value
A	0.3	0.22	−63.0**	18.99
B	0.2	0.34	9.0	14.33
C	−0.5	0.58	−44.0	24.95

** Significant at the 0.01 probability level.

The parameters A, B, and C will each equal zero within the limits of sampling error if the additive-dominance model without the complication of gene interaction is adequate, according to Mather and Jinks[27]. In the present study, the data on amylographic breakdown viscosity, as presented in Table 2, showed a highly significant value for parameter A. However, values of parameters B and C were not significant. On the other hand, all parameters for amylose content were not significant. These indicated that the additive-dominance model was perfectly adequate to describe the amylose content of milled rice in this set of data, and, on the other hand, it was inadequate for the set of data on amylographic breakdown viscosity of milled rice flour.

The Joint Scaling Test

A procedure known as the joint scaling test was further followed to estimate the parameters, m, [d] , and [h] from the various generation means followed by a comparison of the observed generation means with the expected values derived from estimates of the three parameters.

Tables 3, 4, and 5 presented three pieces of important information about the joint scaling test for these two endosperm characteristics. A brief explanation about the data was given as the follows. The weights in Tables 3 and 4 are the reciprocals of the squared standard errors of the means which have been enumerated in Table 1. For example, the weight, 125.12, for Guichow, as shown in Table 3, was caluclated from $125.12=1/(0.0894)^2$. The expected generation mean for Guichow (Table 3) was $26.8=1\times(24.1)+1\times(2.7)+0\times(1)$, where the numbers in each parenthesis are the values of m, [d] , and [h] that were enumerataed in Table 5, respectively, and the coefficients are obtained from Table 3. The Chi-square(X^2) value for amylographic breakdown viscosity, as shown in Table 5, was $13.186=(330-318)^2\times0.0180+(187-212)^2\times0.0135+\cdots\cdots+(32-32)^2\times0.0969$, where all coefficients were presented in Table 4, and in each parenthesis the first one is the observed generation mean and the second one is the expected generation mean.

Table 3. The joint scaling test for amylose content in the Guichow/Lemont crosses.

Generation	Weight	m	[d]	[h]		Observed generation mean	Expected generation mean
Guichow	125.12	1	1	0	=	26.7	26.8
F_1/Guichow	108.70	1	0.5	0.5	=	26.0	26.0
F_1(Guichow/Lemont)	200.06	1	0	1	=	25.0	25.1
F_2	88.50	1	0	0.5	=	24.4	24.6
F_1/Lemont	44.64	1	-0.5	0.5	=	23.3	23.3
Lemont	57.14	1	-1	0	=	24.1	21.4

Table 4. The joint scaling test for amylographic breakdown viscosity in the Guichow/Lemont crosses.

Generation	Weight	m	[d]	[h]		Observed generation mean	Expected generation mean
Lemont	0.0180	1	1	0	=	330	318
F_1/Lemont	0.0135	1	0.5	0.5	=	187	212
F_1(Guichow/Lemont)	0.1258	1	0	1	=	107	106
F_2	0.0305	1	0	0.5	=	133	140
F_1/Guichow	0.0214	1	-0.5	0.5	=	74	69
Guichow	0.0969	1	-1	0	=	32	32

Table 5. The results of the joint scaling test for amylose content and amylographic breakdown viscosity in the Guichow/Lemont crosses.

	Amylose content		Amylographic breakdown viscosity	
	Value	Standard error of the value	Value	Standard error of the value
m(mp)	24.1**	0.007	175**	3.61
[d] (add.)	2.7**	0.007	143**	3.69
[h] (dom.)	1.0**	0.110	-69**	4.79
X^2_3	6.790		13.185	
p	0.10-0.50		0.005-0.001	

** Significant at the 0.01 probability level.

The outcome of these analyses, as shown in Table 5, were completely consistent with the A, B, and C scaling test (Table 2) showing that the additive-dominance model was adequate to describe the data on amylose content, but was inadequate to describe the data on amylographic breakdown viscosity. Thus, the estimates of m, [d] , and [h] for amylographic breakdown viscosity would be biased to an unknown extent by the effects not attributable to the additive-dominance action of the genes.

For these two endosperm characteristics, the estimates of [d] and [h] were significantly different from zero. Both [d] and [h] for amylose content of milled rice were all positive and the value of [d], however, was almost three times as large as [h]. This indicated that the inheritance was mainly controlled by additive genes although dominant genes were also present. Furthermore the gene producing high amylose content were dominant. However, since the additive-dominance model was inadequate to describe the data on amylographic breakdown viscosity, a description of its genetic system could not be given here.

The Six-Parameter Digenic Epistasis Model

The presence of non-allelic interaction for amylographic breakdown viscosity was deduced from the failure to observe the expected relationships between generation means that were required to fit an additive-dominance model by either the individual scaling test (Table 2) or the joint scaling test (Table 5). Therefore a six-parameter digenic epistasis model, thus, was further used to detect the three types of epistatic gene effects. The estimates of the six parameters and their standard errors for both endosperm characteristics in the crosses were given in Table 6.

Table 6. Estimates of the additive, dominance and interaction parameters for amylose content and amylographic breakdown viscosity in the Guichow/Lemont crosses.

	Amylose content		Amylographic breakdown viscosity	
	Value	Standard error of the value	Value	Standard error of the value
m(mp)	23.1**	0.60	191.0**	32.02
[d] (add.)	2.7**	0.08	149.0**	16.46
[h] (dom.)	3.5**	1.30	-148.0**	48.17
[i] (add. X add.)	1.0	.038	−10.0	31.76
[i] (add. x dom.)	0.1	0.86	−72.0**	23.46
[l] (dom. x dom.)	-1.5	0.86	64.0	50.59

** Significant at the 0.01 probability level.

The estimates of the interaction parameters for amylose content of milled rice were not significantly different form zero. Therefore, no evidence of nonallelic interactions was observed for this characteristic. These results agreed with the finding obtained from the individual and joint scaling test. However, as shown in Table 6, the values of [d] and [h] were more or less equal which are different from the data presented in Table 5, in which the value of [d] was almost three times as large as [h].

For amylographic breakdown viscosity, the non-allelic interaction parameter [j] was significantly different from zero. Therefore, an additive x dominance gene interaction effect was present. This indicated that an additive-dominance model with non-allelic gene interaction was adequate to describe the genetic system for amylographic breakdown viscosity, which was in complete agreement with the individual and joint scaling test (Tables 2 and 5).

A genetic mechanism for amylographic breakdown viscosity of milled rice by means of analysis of generation means from mating Guichow with Lemont could be explained as follows. As shown in Table 6, the estimates of [d] and [h] were significantly different from zero, [h] was negative, and the values of [d] and [h] were more or less equal, indicating that dominance was definitely present and the gene producing low amylographic breakdown viscosity was dominant (Table 6). Furthermore, the failure of the fit with an additive-dominance model without the complication of gene interaction was mainly due to the existence of an additive x dominance gene effect [j] .

Genetic Information about Amylose Content Deduced from the Frequency Distributions

The frequency distributions of amylose content for these six populations were plotted in Fig. 2. The patterns of these distributions showed a good fit to the genetic hypothesis of a single incompletely dominance gene conditioning high amylose content. The procedures leading to this deduction were presented as ofllows. The dividing point between high and intermediate amylose level was establisthe at 23% for these populations. For the F_2 population, 63 plants falling into an intermediate amylose content group and 237 plants having high amylose content, indicated a satisfactory fit to a 3 high: 1 intermediate segregation ratio ($X^2=2.56$, $P<0.05$). In the F_1/Guichow population, all the plants fell into the high amylose class, indicating an excellent fit to the genetic hypothesis. In the F_1/Lemont population, the data showed 70 high: 50 intermediate segregation ratio, which gives a good fit to a 1 high:1 intermediate segregation ratio ($X^2=3.33<X^2_{0.05,1}=4.841$).

Genetic Information about Amylographic Breakdown Viscosity Deduced from the Frequency Distributions

The frequency distributions of these six populations for amylographic breakdown viscosity were plotted in Fig. 3. Among these, contrast to amylose content, as shown in Fig. 2, the parents and their hybrid (F_1) showed continuous and unimodal curves. The patterns of these distributions appeared to be near normal, as shown in Fig. 3. However, the patterns of the remaining populations were also continuous but appeared to be multiple-modal.

In general, the frequency distribution of the F_2 population was intermediate between the two parents although transgressive segregation for low amylographic breakdown viscosity was also observed. The frequency distribution of F_1/Guichow population, however, tended toward the relatively low amylographic breakdown viscosity parent, recurrent parent Guichow. On the other hand, the frequency distribution of the F_1/Lemont population showed slightly toward the high amylographic breakdown viscosity parent, recurrent parent Lemont. These indicated an interesting phenomenon. That is, the pollen-parent effect on the shift of the distribution pattern was dramatic.

The segregation in the F_2 population did not show a bimodal distribution. Instead, a multiple-modal curve was observed. However, when 185 BU was used as the divider between low and high amylographic breakdown viscosity, 214 plants fell into a relatively low amylo -

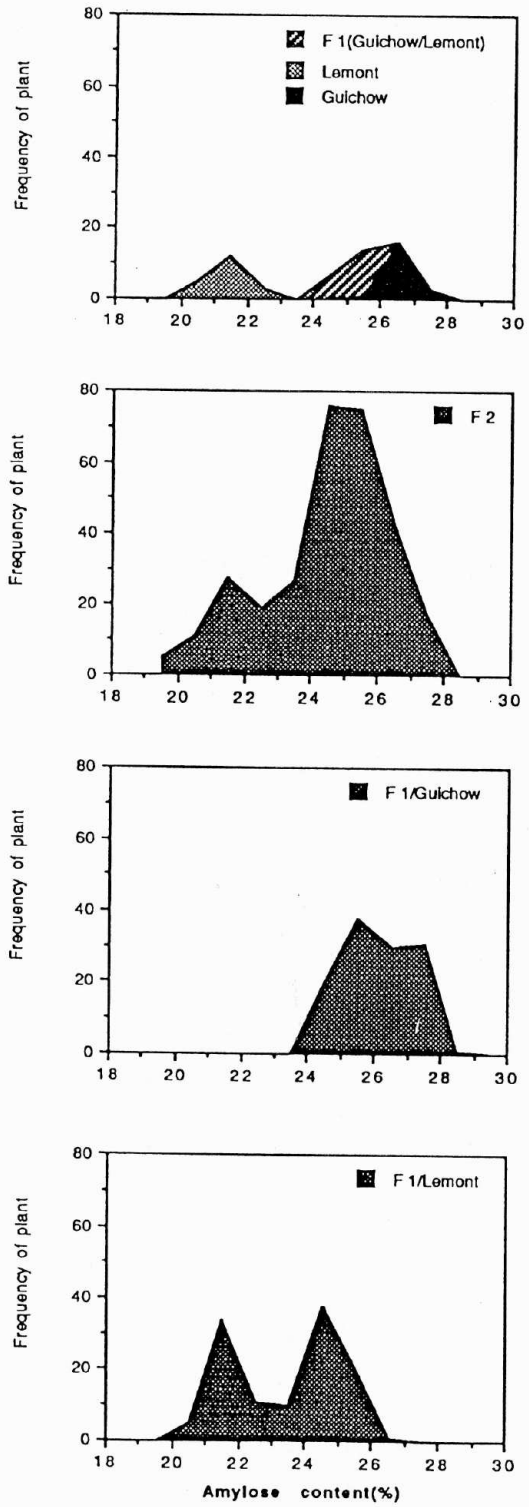

Fig. 2. Frequency distributions of amylose content in the Guichow/Lemont crosses.

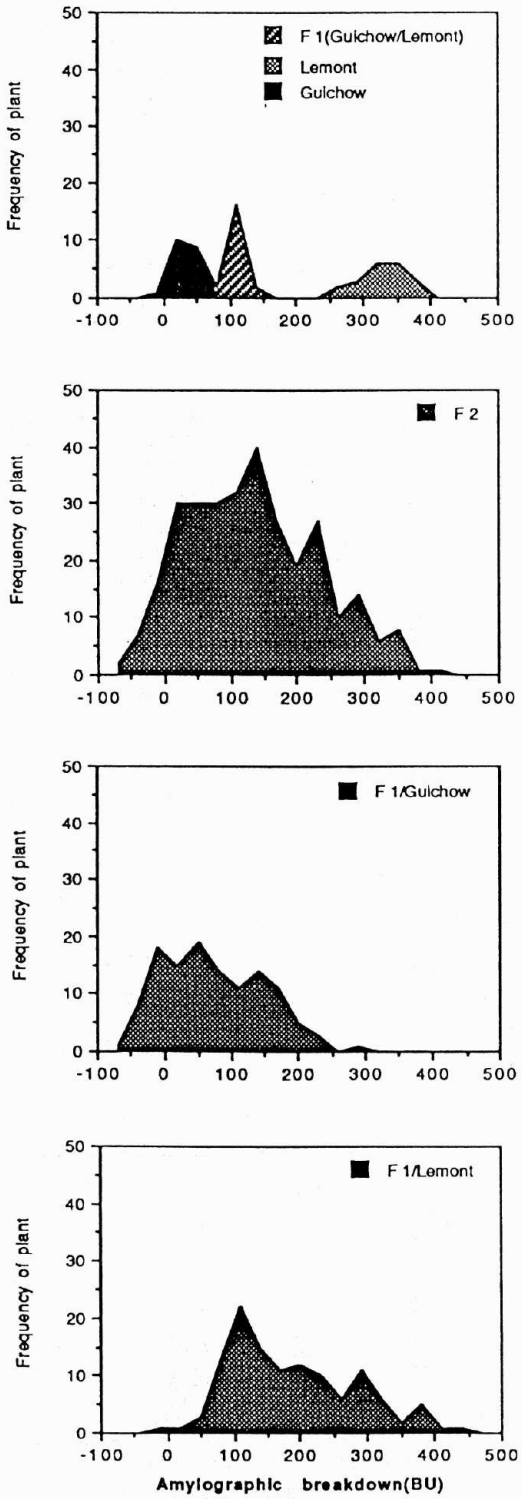

Fig. 3. Frequency distributions of amylographic breakdown viscosity in the Guichow/Lemont crosses.

graphic breakdown viscosity class and 86 plants had a high amylographic breakdown viscosity. This figure showed an approximately 3 low: 1 high segregation ratio for this F_2 population. The genetic hypothesis of a single incompletely dominance gene conditioning low amylographic breakdown viscosity was tested. The Chi-square value ($X^2=1.99$, $P<0.05$) indicated a good fit to a 3 low: 1 high segregation ratio.

Following this genetic hypothesis, the F_1/Lemont population showed 66 low:54 high segregation ratio, indicating a very good fit ($X^2=1.2$, $P<0.05$).But, the genetic hypothesis of a single incompletely dominant gene conditioning low amylographic breakdown viscosity did not hold in the F_1/Guichow population. That is, in the present case, a segregation ratio of 111 low : 9 high was observed which did not fit a 120 low:0 high ratio.

Thus, genetic information about amylose content derived from these six populations produced by mating Guichow with Lemont was different from that found for amylographic breakdown viscosity. This suggests that genetic mechanism conditioning amylose content and amylographic breakdown viscosity might not be the same.

DISCUSSION

The amylose content of the grains of a rice plant can be seen as the result of interaction between environmental factors and genetic properties[10]. Among the different environmental factors affecting amylose content, the temperature during grain ripening is the dominant factor, followed by nitrogen fertilization and the degree of milling. Cooler environmental temperature increases amylose content[1,2,3,30,36]. Amylose content of rice decreased slightly with increasing nitrogen fertilization but was not affected by the stage at which nitrogen was applied[30]. Amylose content also increased with an increasing in the degree of milling. There is some variation between individual rice plants, between panicles within a plant[30],and between kernels within a panicle[44]. Since variation in amylose content between plants was much less (2%) than than between panicles within plants (3 to 7%), the use of bulk samples for amylose content determination has been recommended[30]. Hence, uniform and standard techniques for the determination of amylose content of rice are desirable[10].

Up to now, the traditional method used in most genetic studies on amylose content in rice was based on bulk seed analysis of genetically heterozygous plants. For example, F_1 and F_2 plant values are represented by bulk F_2 and F_3 endosperm populations, respectively. Kumar and Khush[18] argued that analysis of the bulk seed samples of genetically heterozygous plants provided biased information on the inheritance of amylose content. However, data on amylose content obtained using single-grain analysis were undoubtedly confounded by the variation between grains within a panicle and between panicles within a plant as well as by differences in genetic properties[22,23,24,25]. Most of the published reports, based on bulk seed analysis, indicated that high amylose content is incompletely dominant to low content and is controlled by one major gene and several modifiers[4,7,8,28,35]. The role of two complementary genes was indicated in some studies[12,28,36]. The genetic system deduced from the observation of the distributions of amylose content in F_2 populations indicated typical quanitiative inheritance[4,20]. Both additive and dominant effects are impor

tant[17,21,34] and additive effects are significantly larger than dominant effects in affecting amylose content[21], a conclusion from a diallel andlysis. Transgressive segregation for amylose content is indicated in some studies[4,9,28,35], but not observes in another study[7,36]. The role of dosage effects might or might not exist, depending on materials used[13,18]. If intermediate amylose content is desired, one or both parents should be intermediate[14]. In contrast, Kumar and Khush[18], using single-grain analysis, found that the genes for high amylose content are completely dominant over those for low or intermediate amylose content and is controlled by a single major gene and modifiers. In present study, genetic information about amylose content derived from these six populations produced by mating Guichow with Lemont is simliar to most of published reports and different from the data of Kumar and Khush[18]. That is, our data suggested that the genes for high amylose content are incompletely dominant over intermediate amylose content and is controlled by a single major gene. This might be partly from a sample determination basis, i.e., bulk seed versus single -grain, and partly from materials having different genetic background mentioned above.

The most important physical property of starch is its ability to swell and produce a viscous paste when heated in water. The amylographic viscosity measurements, a physical index of rice starch, vary according to the sources of starches[11]. Amylographic paste viscosity characteristics of the typical U. S. long-grain cultivars usually show an intermediate peak viscosity, relatively high breakdown viscosity, and a slightly positive setback viscosity. In contrast, amylograms of the typical U. S. medium-and short-grain cultivars usually show a comparatively low cooled-paste viscosity[39,41,43,45]. A superior cooking and processing U. S. long-grain type is characterized by an amylose content 2-4% higher than that of typical U. S. long-grain type and a much low amylographic breakdown viscosity, indicative of low loss of solids and little splitting and fraying of edges and ends in canning [5,6,40,43]. Scientists in Japan found that peak viscosity and breakdown values of rice flour tended to increase from the northeast to the southwest regions[37]. Amylographic peak viscosity of rice flour increased during storage at ambient temperature, but no peak viscosity increase was found in samples stored at low temperature[37]. That amylographic peak viscosity values were consistently lower for ratoon-crop samples was also observed in the United States[46]. Published results from Taiwan clearly and definitely indicated that highly signifficant correlation exists between amylographic viscosity measurements and eating quality[26].

Since amylographic breakdown viscosity was considered particularly useful in evaluating rice for canning quality and the run was time-consuming, an abridged amylographic method, performed with 50 g ground rice flour, starting temperature of 60°C, reducing the cooking time at 95°C to 10 minuts, and eliminating the cooking cycle phase of the curve, was suggested to meet the testing of a relatively large number of breeding lines[42]. However, up to now, genetic study on amylographic breakdown viscosity has not been conducted simply because the sample unit is difficult to meet. In this study, a small-sample size abridged amylographic profile was run, data of amylographic breakdown viscosity were figured out

and its genetic information was infferred. It was found that the genetic hypothesis inferred in the present paper was similar to the previous paper[24], that was deduced from a diallel graph analysis based on regular amylographic viscosity measurement, i. e. a sample size of 50 g ground rice flour.

In conclusion, compared with other plant quantitative characteristics such as plant height, panicle length, etc., a satisfactory quantitative genetic model and grain composition determining technique based on single-grain basis for endosperm characteristics have not yet been developed although much attention has recently been devoted to the grain quality. The lack of proper genetic model and composition determining technique baaed on single -grain basis have been an obstacle in studying the inheritance of endosperm characteristics [29]. Therefore, establishing a quantitative genetic model and innovating the composition determining technique for endosperm characteristics will be of benefit to breeding programs in cereal crops of which high grain quality is a priority.

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白米直鏈澱粉含量與澱粉糊崩解黏度之世代平均值法遺傳研究[1]

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摘 要

直鏈澱粉含量及澱粉糊崩解黏度是稻米食用與加工品質判定的重要指標。本研究以 Guichow 及 Lemont 爲親本所建構成之 P_1、P_2、F_1、F_2、BC_1 及 BC_2 等六個族群爲材料，進行稻米直鏈澱粉含量及澱粉糊崩解黏度之遺傳研究。經由世代平均值之分析推得直鏈澱粉含量之遺傳符合累加性-顯性之遺傳機制，而澱粉糊崩解黏度則未符合累加性-顯性之遺傳機制。直鏈澱粉含量方面，在累加性及顯性等兩種基因效應中，是以累加性效應較強，而高直鏈澱粉含量是爲顯性。而澱粉糊崩解黏度除累加性及顯性等兩種基因效應外，尚發現有累加性×顯性交感存在，其中，累加性及顯性等兩種基因效應約相等，而低澱粉糊崩解黏度爲顯性。由各後裔族群各該性狀頻度分布之觀察與卡方測定之結果則指出：高直鏈澱粉含量由一對不完全顯性基因所控制；而澱粉糊崩解黏度則未能符合一對不完全顯性基因控制之遺傳假說。

關鍵詞：直鏈澱粉含量、澱粉糊崩解黏度、白米、世代平均值。

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